

## EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	2	"20050130171"	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/01/23 10:17
S1	48395	bodary.in. or clark.in. or hunt.in. or jackman.in.	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/01/23 09:04
S2	3588	(\$array\$2 or \$5chipo\$2 or immobili\$) and S1	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/01/23 09:05
S3	1818588	(\$array\$2 or \$5chip\$2 or immobili\$)	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/01/23 09:06
S4	483	immune adj relate\$ adj disorder	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/01/23 09:06
S5	10	S1 and S3 and S4	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/01/23 10:17

**SCORE Search Results Details for Application  
10527100 and Search Result  
20070112\_105344\_us-10-527-100a-1.rng.**

Comments /  
Suggestions

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GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

```
Run on:      January 12, 2007, 18:43:29 ; Search time 1280 Seconds
              (without alignments)
              10834.220 Million cell updates/sec
```

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Title:          US-10-527-100A-1
Perfect score:  1989
Sequence:       1 ggcacgagggcggtcacgggc.....ttaaaaaaaaaaaaaaaaaaaaa 1989
```

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database : N_Geneseq_8:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	1989	100.0	1989	12	ADL91486	Adl91486 Human imm
2	1975	99.3	3425	14	ADY20185	Ady20185 DNA encod
3	1973.4	99.2	2834	12	ADI61675	Adi61675 Human cDN
4	1973.4	99.2	2834	14	AEA43840	Aea43840 Human cDN
5	1939	97.5	2032	10	ADD29570	Add29570 Human tum
6	1939	97.5	2032	10	ADA53766	Ada53766 Human cod
7	1930	97.0	2000	6	ABQ60910	Abq60910 Clone IMA
8	1741.8	87.6	1911	13	ACN39899	Acn39899 Tumour-as
c 9	1359.6	68.4	149480	6	ABL61947	Abl61947 Colon ade
c 10	1359.6	68.4	149480	6	ABL68365	Abl68365 Kidney ca
c 11	1359.6	68.4	149480	6	ABL61948	Abl61948 Colon ade
12	762.4	38.3	1162	8	ABZ57031	Abz57031 Human kin
c 13	664.8	33.4	854	13	ADR26106	Adr26106 Breast ca
c 14	642.2	32.3	819	14	AEB35205	Aeb35205 Human Gef
15	597	30.0	2971	5	AAS84667	Aas84667 DNA encod
16	517	26.0	590	9	ACH40628	Ach40628 Human foe
17	479	24.1	1181	4	AAS27166	Aas27166 cDNA enco
18	479	24.1	1181	4	ABK43848	Abk43848 DNA encod
19	479	24.1	1181	5	AAS34308	Aas34308 Human cDN
20	479	24.1	1181	10	ADB93344	Adb93344 Human cDN
21	479	24.1	1181	12	ADI54235	Adi54235 cDNA enco
22	465	23.4	518	9	ACH38122	Ach38122 Human end
23	372.6	18.7	445	9	ACH41694	Ach41694 Human foe
24	318.8	16.0	636	5	AAS84665	Aas84665 DNA encod
25	263.6	13.3	600	14	AEE14026	Aee14026 Hamster c
26	261.4	13.1	586	14	AEE17668	Aee17668 Hamster S
27	258.4	13.0	274	2	AAT24451	Aat24451 Human gen
28	203	10.2	277	13	ADU10968	Adu10968 Solid tum
29	122.6	6.2	560	12	ACH74342	Ach74342 Human gen
30	115	5.8	115	12	ACH88042	Ach88042 Human gen
31	107.8	5.4	452	5	AAS84666	Aas84666 DNA encod
32	89	4.5	129	3	AAC14427	Aac14427 Human sec
33	74.2	3.7	6036	12	ADM66990	Adm66990 Human hom
34	74.2	3.7	6050	13	ACN40874	Acn40874 Tumour-as
35	74.2	3.7	6170	5	AAS44966	Aas44966 cDNA enco
36	74.2	3.7	6351	5	AAS45154	Aas45154 cDNA enco
37	74.2	3.7	6573	10	ADI60598	Adi60598 Secreted
38	74.2	3.7	8977	10	ADE48299	Ade48299 Human MIC
39	72.6	3.7	4327	13	ADR06825	Adr06825 Full leng
c 40	70	3.5	2000	8	ADA71938	Ada71938 Rice gene
41	70	3.5	3827	12	ADM66989	Adm66989 Murine ad
42	68.8	3.5	428	8	ABX53847	Abx53847 Bovine ES
43	58.2	2.9	1869	13	ADR07616	Adr07616 Full leng
44	58.2	2.9	2134	3	AAA08112	Aaa08112 Human bla
45	58.2	2.9	2224	10	ADC32017	Adc32017 Human nov

## ALIGNMENTS

ADI61675

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Best Local Similarity 99.9%; Pred. No. 0;

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Qy	130	AATTAAAGCAATCTTTGTCCACCCATCTGGAAGCCGAGAAGCCTCTGAGGCGCTATGGGG	189
Db	639	AATTAAAGCAATCTTTGTCCACCCATCTGGAAGCCGAGAAGCCTCTGAGGCGCTATGGGG	698
Qy	190	CGGTGGAGGAGACGGCTTGAAAAACGGAGAGACTGGGGAGAAATCAGCTGGACATCATCT	249
Db	699	CGGTGGAGGAGACGGCTTGAAAAACGGAGAGACTGGGGAGAAATCAGCTGGACATCATCT	758
Qy	250	CCATGGCGGAGACAACCATGATGCCAGAGGAGATTGAGCTGGAGATGGCAAAAATTCAGC	309
Db	759	CCATGGCGGAGACAACCATGATGCCAGAGGAGATTGAGCTGGAGATGGCAAAAATTCAGC	818
Qy	310	GTCTCCGGGAAGTCTTGGTCCGCCGGGAGTCTGAGCTCAGGTTTCATGATGGATGACATCC	369
Db	819	GTCTCCGGGAAGTCTTGGTCCGCCGGGAGTCTGAGCTCAGGTTTCATGATGGATGACATCC	878
Qy	370	AGCTCTGCAAGGACATCATGGACTTGAAGCAGGAGCTGCAGAACTTGGTCGCCATCCCAG	429
Db	879	AGCTCTGCAAGGACATCATGGACTTGAAGCAGGAGCTGCAGAACTTGGTCGCCATCCCAG	938
Qy	430	AAAAAGAAAAAACCAAACCTGCAGAAGCAGAGAGAGGATGAGCTAATCCAGAAGATCCACA	489
Db	939	AAAAAGAAAAAACCAAACCTGCAGAAGCAGAGAGAGGATGAGCTAATCCAGAAGATCCACA	998
Qy	490	AACTGGTGCAAGAAGAGAGACTTCCTGGTGGACGATGCGGAGGTCGAGCGGTTAAGGGAGC	549
Db	999	AACTGGTGCAAGAAGAGAGACTTCCTGGTGGACGATGCGGAGGTCGAGCGGTTAAGGGAGC	1058
Qy	550	AAGAAGAAGACAAGGAAATGGCTGATTTCTTGAGAATCAAGTTAAACCTCTAGACAAAG	609
Db	1059	AAGAAGAAGACAAGGAAATGGCTGATTTCTTGAGAATCAAGTTAAACCTCTAGACAAAG	1118
Qy	610	TAACCAAATCTCCAGCCAGCTCCCGGGCAGAGAAGAAAGCAGAGCCCCACCTAGCAAGC	669
Db	1119	TAACCAAATCTCCAGCCAGCTCCCGGGCAGAGAAGAAAGCAGAGCCCCACCTAGCAAGC	1178
Qy	670	CCACGGTGGCCAAGACGGGGCTGGCACTGATCAAGGATTGTTGCGGGGCCACCCAGTGCA	729
Db	1179	CCACGGTGGCCAAGACGGGGCTGGCATTGATCAAGGATTGTTGCGGGGCCACCCAGTGCA	1238
Qy	730	ACATCATGTAGCCCCACGTGGGGTGCCCTGGGCCATGGGGACCCCCCCCCACCTCTTG	789
Db	1239	ACATCATGTAGCCCCACGTGGGGTGCCCTGGGCCATGGGGACCCCCCCCCACCTCTTG	1298
Qy	790	TCTTTATAGCCCCATTTACCGGGGCCAAGAGCTCTCCAAGGCAGAAGGGGTTGAAGG	849
Db	1299	TCTTTATAGCCCCATTTACCGGGGCCAAGAGCTCTCCAAGGCAGAAGGGGTTGAAGG	1358
Qy	850	CAAGCCCGTGACTGTCAACAGAGGCCATGGGCACGGCAGGCGGGCCTGGCCACCCTGTAC	909
Db	1359	CAAGCCCGTGACTGTCAACAGAGGCCATGGGCACGGCAGGCGGGCCTGGCCACCCTGTAC	1418
Qy	910	AGAGTGTAGCAGTAGGGAGTCTCTCACCGTCGCATGGTCCTCCCCAGAGCATGCCGAACC	969
Db	1419	AGAGTGTAGCAGTAGGGAGTCTCTCACCGTCGCATGGTCCTCCCCAGAGCATGCCGAACC	1478
Qy	970	CAGGAGTCTGTCTCACTGTTTATCCAAACACCAGGAAAGGTCTCCCTCAAAAAAGCATA	1029
Db	1479	CAGGAGTCTGTCTCACTGTTTATCCAAACACCAGGAAAGGTCTCCCTCAAAAAAGCATA	1538
Qy	1030	TCTCCACTTCTCTCTAGCTGTATCTAACCACCGTGTGAATGAACTGGGAGAGGGGCATG	1089

Db	1539	TCTCCACTTCTCTCTAGCTGTATCTAACCACCGTGTGAATGAACTGGGAGAGGGGCATG	1598
Qy	1090	CTCCCCAGCTGTGTGTAGTTCGTGACTTCTCAACAATCTAGCACCATGTTCGGACACGTTCC	1149
Db	1599	CTCCCCAGCTGTGTGTAGTTCGTGACTTCTCAACAATCTAGCACCATGTTCGGACACGTTCC	1658
Qy	1150	CCATCCACCCTCCTAGCTCTGCTCTCAGAGCTAGGCACATGGGCACAGGTCCCCTCCCGT	1209
Db	1659	CCATCCACCCTCCTAGCTCTGCTCTCAGAGCTAGGCACATGGGCACAGGTCCCCTCCCGT	1718
Qy	1210	CTGTCTCTCTCCAGCAACTGTGCCCTGGAGGGCTCCACATGGCCCCCGTGTCTCTCGGGC	1269
Db	1719	CTGTCTCTCTCCAGCAACTGTGCCCTGGAGGGCTCCACATGGCCCCCGTGTCTCTCGGGC	1778
Qy	1270	ACCACCCATATAGCAGTCCCAGAGGGCCCATCTGTAAAGATCGAGCTTGTGTGTGGTGTC	1329
Db	1779	ACCACCCATATAGCAGTCCCAGAGGGCCCATCTGTAAAGATCGAGCTTGTGTGTGGTGTC	1838
Qy	1330	GTGGTCACATCTCCCGCTTCCCCCATCCTGTGTCTGGGCACAGTTCACATCAGGACAGC	1389
Db	1839	GTGGTCACATCTCCCGCTTCCCCCATCCTGTGTCTGGGCACAGTTCACATCAGGACAGC	1898
Qy	1390	GTCCATTGTGCTCTCAGTCTGCCTCAGGTGTGTGCCTGGAGGGGGCCTGGACTGGCATGG	1449
Db	1899	GTCCATTGTGCTCTCAGTCTGCCTCAGGTGTGTGCCTGGAGGGGGCCTGGACTGGCATGG	1958
Qy	1450	ATCCAGTGTGCAGAAGAGCCAGCAGGGAACCGGAAGCTCTGATGTCAAGGCCAGAGCAGT	1509
Db	1959	ATCCAGTGTGCAGAAGAGCCAGCAGGGAACCGGAAGCTCTGATGTCAAGGCCAGAGCAGT	2018
Qy	1510	TGAGAATGGGACCCAGAGTAGATGCTGACCTGGGCACTCCACCATTCCGGGGCCACCACA	1569
Db	2019	TGAGAATGGGACCCAGAGTAGATGCTGACCTGGGCACTCCACCATTCCGGGGCCACCACA	2078
Qy	1570	GAGATGCCAGCAGGATGCCACTTTGCCAGCCCGACACACGGACCTTTGTAAAGAACAGCA	1629
Db	2079	GAGATGCCAGCAGGATGCCACTTTGCCAGCCCGACACACGGACCTTTGTAAAGAACAGCA	2138
Qy	1630	ACAGGCAGGAGAGGCAGCGTGTGACCAGATTGTGTCCCGTCATTGGGTGGCATATGTTAA	1689
Db	2139	ACAGGCAGGAGAGGCAGCGTGTGACCAGATTGTGTCCCGTCATTGGGTGGCATATGTTAA	2198
Qy	1690	CTAGCTGCCAAACAACCTTCAACCCGTGTAATTCATGTACATTTGCAACAGCCAGCCCGGT	1749
Db	2199	CTAGCTGCCAAACAACCTTCAACCCGTGTAATTCATGTACATTTGCAACAGCCAGCCCGGT	2258
Qy	1750	ACAGCCTGTGTGACTTCTCTGTATGTGTGTGTGTGTGTCGTGACCAGCCTAAGTAGTTAGCA	1809
Db	2259	ACAGCCTGTGTGACTTCTCTGTATGTGTGTGTGTGTGTCGTGACCAGCCTAAGTAGTTAGCA	2318
Qy	1810	TAACTCAAGATGCTGATGTGCAGTCACCCATCAGAGAAAATAAAAATGGAAACCACGTTTC	1869
Db	2319	TAACTCAAGATGCTGATGTGCAGTCACCCATCAGAGAAAATAAAAATGGAAACCACGTTTC	2378
Qy	1870	ACAGCATTTTAAAGTTTTTACTTTTTTTCTTGATTATGGAAGTAATCCATGTACATAGT	1929
Db	2379	ACAGCATTTTAAAGTTTTTACTTTTTTTCTTGATTATGGAAGTAATCCATGTACATAGT	2438
Qy	1930	AAATCATTTTAAAGTACAAAAGTATGAAGAAGTTTGTCTTAAAAAAAAAAAAA	1984

Db 2439 AAATCATTTTAAAAAGTACAAAAAGTATGAAGAAGTTTGTCTTAAAAAAAAAAAAA 2493

<!--EndFragment-->